GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 24, 2004, 13:44:25 ; Search time 125 Seconds
(without alignments)
560.574 Million cell updates/sec

Title: US-09-554-465-75
Perfect score: 1324
Sequence: 1 EVQLLEQSGAELVRPGTSVK.....CQNDYSYPLTFGAGTKLEIK 248

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1324	100.0	248	2	AAY17964	Aay17964 Mouse scF
2	1261	95.2	248	2	AAY17960	Aay17960 Mouse scF
3	1203	90.9	248	2	AAY17965	Aay17965 Mouse scF
4	1177	88.9	258	5	AAU72865	Aau72865 P5-2 sing
5	1060	80.1	242	2	AAY17959	Aay17959 Mouse scF
6	1057	79.8	242	2	AAY17957	Aay17957 Mouse scF
7	1054	79.6	242	2	AAY17961	Aay17961 Mouse scF
8	1027	77.6	258	5	AAU72871	Aau72871 3B10xP4-3
9	1027	77.6	505	5	AAU72875	Aau72875 Human NKG
10	1022	77.2	288	2	AAW82743	Aaw82743 Fusion pr
11	1022	77.2	673	2	AAW82742	Aaw82742 Plasmid p
12	1009	76.2	242	4	AAB31422	Aab31422 Protein u
13	1004.5	75.9	262	4	AAB31421	Aab31421 Protein u
14	995.5	75.2	500	7	ADD13792	Add13792 Plasmid p
15	990.5	74.8	255	5	AAU72870	Aau72870 P5-23 sin
16	988.5	74.7	271	4	AAB31423	Aab31423 Protein u
17	988	74.6	272	4	AAB31424	Aab31424 Protein u
18	978.5	73.9	259	5	AAU72862	Aau72862 P4-3 sing
19	978	73.9	444	6	ABJ39018	Abj39018 CC49 sing
20	972	73.4	532	2	AAW35565	Aaw35565 HindIII-E
21	956	72.2	580	2	AAW90217	Aaw90217 Bispecifi
22	953	72.0	556	2	AAW90218	Aaw90218 Bispecifi
23	940.5	71.0	251	2	AAY17958	Aay17958 Mouse scF
24	935.5	70.7	251	2	AAY17962	Aay17962 Mouse scF
25	935.5	70.7	507	5	AAU72858	Aau72858 8G7C10x4-
26	935.5	70.7	510	5	AAU72859	Aau72859 6E5A7x4-7
27	935.5	70.7	510	5	AAU72860	Aau72860 Human p53
28	935.5	70.7	532	3	AAY78328	Aay78328 Bispecifi
29	921	69.6	249	2	AAW60770	Aaw60770 Single ch
30	914	69.0	543	7	ADD12876	Add12876 CD28/mela
31	908.5	68.6	291	4	AAB20443	Aab20443 Antibody
32	908.5	68.6	322	4	AAB20440	Aab20440 Antibody
33	908.5	68.6	729	4	AAB20439	Aab20439 Antibody
34	905	68.4	282	2	AAW09818	Aaw09818 VH4715-li
35	905	68.4	282	2	AAW35564	Aaw35564 HindIII-E
36	905	68.4	355	2	AAW35133	Aaw35133 R. pipien
37	902	68.1	483	2	AAW88099	Aaw88099 A protein
38	902	68.1	483	3	AAB07935	Aab07935 A divalen
39	902	68.1	483	3	AAY57254	Aay57254 Divalent
40	902	68.1	483	3	AAB27679	Aab27679 Bivalent
41	902	68.1	483	3	AAY80924	Aay80924 Bivalent
42	902	68.1	483	6	ABU61809	Abu61809 Divalent
43	902	68.1	486	2	AAR37649	Aar37649 Sequence
44	898.5	67.9	392	3	AAB10863	Aab10863 S11-VEGF2
45	898.5	67.9	510	3	AAB10864	Aab10864 S11-scVEG

ALIGNMENTS

RESULT 1
AAY17964
ID AAY17964 standard; protein; 248 AA.
XX
AC AAY17964;
XX
DT 04-AUG-1999 (first entry)
XX
DE Mouse scFV fragment 5-10.
XX
KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW autoimmune disease; scFv-antibody; single-chain Fv; mouse.
XX
OS Mus sp.
XX
PN WO9925818-A1.
XX
PD 27-MAY-1999.
XX
PF 16-NOV-1998; 98WO-EP007313.
XX
PR 17-NOV-1997; 97EP-00120096.
XX
PA (KUFE/) KUFER P.
XX
PI Kufer P, Raum T, Borschert K, Zettl F, Lutterbuese R;
XX
DR WPI; 1999-338004/28.
DR N-PSDB; AAX77247.
XX
PT Phage display system for identification of binding site domains retaining
PT capacity to bind an epitope.
XX
PS Claim 27; Fig 6.10; 152pp; English.
XX
CC The invention relates to a method of identifying binding site domains
CC (BSD) that retain the capacity of binding to a predetermined epitope when
CC positioned C-terminal of at least one further domain in a recombinant bi-
CC or multivalent polypeptide. The method comprises (a) testing a panel of
CC BSD displayed on the surface of a biological display system as part of a
CC fusion protein for binding to a predetermined epitope, where the fusion
CC protein comprises an additional domain positioned N-terminal of the BSD
CC and an amino acid sequence that mediates anchoring of the fusion protein
CC to the surface of the display system; and (b) identifying a BSD that
CC binds to the predetermined epitope. The method is useful to identify bi-
CC or multivalent polypeptides that comprise antibody binding sites capable
CC of efficiently binding to the corresponding antigen. The polypeptides or
CC antibodies identified by the method are useful therapeutically and

Applicant 1

CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
CC fragments that bind independently of their position within bifunctional
CC single-chain fusion proteins can be isolated from combinatorial antibody
CC libraries using the new in vitro method. Sequences AAY17957-965 represent
CC mouse scFV fragments
XX
SQ Sequence 248 AA;

Query Match 100.0%; Score 1324; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.7e-87;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 EVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDIFPGSGNIH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDIFPGSGNIH 60

Qy         61 YNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQGTTVTVSS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQGTTVTVSS 120

Qy        121 GGGGSGGGGSGGGGSELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGGSGGGGSGGGGSELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQK 180

Qy        181 PGQPPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PGQPPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFG 240

Qy        241 AGTKLEIK 248
              ||||||||
Db        241 AGTKLEIK 248
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RESULT 2
AAY17960
ID AAY17960 standard; protein; 248 AA.
XX
AC AAY17960;
XX
DT 04-AUG-1999 (first entry)
XX
DE Mouse scFV fragment 4-1.
XX
KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW autoimmune disease; scFv-antibody; single-chain Fv; mouse.
XX
OS Mus sp.
XX
PN WO9925818-A1.
XX
PD 27-MAY-1999.
XX
PF 16-NOV-1998; 98WO-EP007313.
XX
PR 17-NOV-1997; 97EP-00120096.
XX
PA (KUFE/) KUFER P.
XX
PI Kufer P, Raum T, Borschert K, Zettl F, Lutterbuese R;
XX
DR WPI; 1999-338004/28.
DR N-PSDB; AAX77243.
XX
PT Phage display system for identification of binding site domains retaining
PT capacity to bind an epitope.
XX
PS Claim 27; Fig 6.6; 152pp; English.
XX
CC The invention relates to a method of identifying binding site domains
CC (BSD) that retain the capacity of binding to a predetermined epitope when
CC positioned C-terminal of at least one further domain in a recombinant bi-
CC or multivalent polypeptide. The method comprises (a) testing a panel of
CC BSD displayed on the surface of a biological display system as part of a
CC fusion protein for binding to a predetermined epitope, where the fusion
CC protein comprises an additional domain positioned N-terminal of the BSD
CC and an amino acid sequence that mediates anchoring of the fusion protein
CC to the surface of the display system; and (b) identifying a BSD that
CC binds to the predetermined epitope. The method is useful to identify bi-
CC or multivalent polypeptides that comprise antibody binding sites capable
CC of efficiently binding to the corresponding antigen. The polypeptides or
CC antibodies identified by the method are useful therapeutically and
CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
CC fragments that bind independently of their position within bifunctional
CC single-chain fusion proteins can be isolated from combinatorial antibody
CC libraries using the new in vitro method. Sequences AAY17957-965 represent
CC mouse scFV fragments
XX
SQ Sequence 248 AA;

Query Match 95.2%; Score 1261; DB 2; Length 248;
Best Local Similarity 95.6%; Pred. No. 9e-83;
Matches 237; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

```
Qy          1 EVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDIFPGSGNIH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||| |
Db          1 EVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWVGDIFPGSGNAH 60

Qy         61 YNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQGTTVTVSS 120
              |||||||||||||||| |||||||||| |||||||||||||||| ||||||||||||||
Db         61 YNEKFKGKATLTADKSSYTAYMQLSSLTSEDSAVYFCARLRNWDEAMDYWGQGTTVTVSS 120

Qy        121 GGGGSGGGGSGGGGSELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQK 180
              ||||||||||||||||||||||||:|:|||||||||||||||||||||| |||||
Db        121 GGGGSGGGGSGGGGSELVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSGNQKNYLAWYQQK 180

Qy        181 PGQPPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPYTFG 240
              |||||||||| |||||||||||||||||||||||||||||||||||||||||| |||
Db        181 PGQPPKLLIYGASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPYTFG 240

Qy        241 AGTKLEIK 248
              ||||||||
Db        241 GGTKLEIK 248
```

RESULT 3
AAY17965
ID AAY17965 standard; protein; 248 AA.
XX
AC AAY17965;
XX
DT 04-AUG-1999 (first entry)
XX
DE Mouse scFV fragment 5-13.
XX
KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW autoimmune disease; scFv-antibody; single-chain Fv; mouse.
XX
OS Mus sp.
XX
PN WO9925818-A1.
XX
PD 27-MAY-1999.
XX
PF 16-NOV-1998; 98WO-EP007313.
XX
PR 17-NOV-1997; 97EP-00120096.
XX
PA (KUFE/) KUFER P.
XX
PI Kufer P, Raum T, Borschert K, Zettl F, Lutterbuese R;
XX
DR WPI; 1999-338004/28.
DR N-PSDB; AAX77248.
XX
PT Phage display system for identification of binding site domains retaining
PT capacity to bind an epitope.